

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: Deutsches Krebsforschungszentrum Stiftung des öffentlichen Rechts
- (B) STREET: Im Neuenheimer Feld 280
- (C) CITY: Heidelberg
- (E) COUNTRY: Germany
- (F) POSTAL CODE: 69120

(ii) TITEL OF INVENTION: DNase active Protein

(iii) NUMBER OF SEQUENCES: 3

(iv) COMPUTER-READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPA)

(v) CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/DE96/01016

(vi) PRIOR APPLICATION DATA:

- (A) APPLICATION DATE: DE 195 21 046.8
- (B) APPLICATION DATE: 09-JUN-1995

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2661 Base pairs
- (B) TYPE: Nucleotide
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) TYPE OF MOLEKULE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 795..1700

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CTTGAACGCC TGACCTCGTA TCCACCCGCC TCAGCCTCCC AAAGTGCTGG GATTACAGGC 60
ATGAGCCACC ACGCCCAGCC CATAATTTAT TGATTTTSTA AAATTTGTCC AGCCTTCTAT 120
TACCACGTCG AATCCATTAG CTACAGCCAT CCCATGAGAA GCTGAGTGGA TTCAGCCCCA 180
CCTCCTGCTC ACAGACCCTG TCCGAGCACC TCATTTGTCC CAACAGCATT ACTGCAGGAC 240

CCCCAGGACG	TTGGACTGCC	AGCTCCCTGG	GTCTCCTCCT	CTCTGGGGCA	GATCCTCAGT	300										
CCTCCCTTGA	CTTCACGACT	GTGGCCAGAT	CATGTGTGGA	CTGTCCCTCT	CTTTGGGTCT	360										
CCAGAGCGCT	TGCATCAAAC	ACCCCTAACT	CAGAAAGTGTG	CAGCCACACT	GGGACTCAGA	420										
ACCCAACAAC	AGGGACAGAA	GACTCACGCC	CTTGGGGTGC	CCGGTCTCGT	GGCATCAGGC	480										
ATGACTTCCA	GCTCCTGCGC	CTTCCCCAGC	AACTGCTGAC	TGGGGACCCA	GACCGGGAGC	540										
TGAGCGACGG	GCCTGGCGAG	CGAAGCTCGG	GGTCTCACTC	AGGCACCAGC	CCCTCCTTGC	600										
CCCAGGCTTG	AGTGACTCAC	AGCCCTATTC	AGGCAGGAGC	TGCTCTTCTG	GGGTATCGCG	660										
ATCCACTTAA	GGATGAGGCA	GACTTGGTGA	CAAGCTGGTC	TGAGCAGCGC	TTCCAGAGCC	720										
AGAACTGAGC	CCAGTGAGAG	CGCACCCCTGG	AGCAGCCTGG	ATTCCTGGGG	TGTCCCCGGC	780										
AGCCACACAC	AGCC	ATG	CAC	TAC	CCA	ACT	GCA	CTC	CTC	TTC	CTC	ATC	CTG	830		
		Met	His	Tyr	Pro	Thr	Ala	Leu	Leu	Phe	Leu	Ile	Leu			
		1				5					10					
GCC	AAT	GGG	GCC	CAG	GCC	TTT	CGC	ATC	TGC	GCC	TTC	AAT	GCC	CAG	CGG	878
Ala	Asn	Gly	Ala	Gln	Ala	Phe	Arg	Ile	Cys	Ala	Phe	Asn	Ala	Gln	Arg	
		15					20					25				
CTG	ACA	CTG	GCC	AAG	GTG	GCC	AGG	GAG	CAG	GTG	ATG	GAC	ACC	TTA	GTT	926
Leu	Thr	Leu	Ala	Lys	Val	Ala	Arg	Glu	Gln	Val	Met	Asp	Thr	Leu	Val	
		30					35				40					
CGG	ATA	CTG	GCT	CGC	TGT	GAC	ATC	ATG	GTG	CTG	CAG	GAG	GTG	GTA	GAC	974
Arg	Ile	Leu	Ala	Arg	Cys	Asp	Ile	Met	Val	Leu	Gln	Glu	Val	Val	Asp	
		45				50				55					60	
TCT	TCC	GGC	AGC	GCC	ATC	CCC	CTC	CTG	CTT	CGA	GAA	CTC	AAT	CGA	TTT	1022
Ser	Ser	Gly	Ser	Ala	Ile	Pro	Leu	Leu	Leu	Arg	Glu	Leu	Asn	Arg	Phe	
					65					70					75	
GAT	GGC	TCT	GGG	CCC	TAC	AGC	ACC	CTG	AGC	AGC	CCC	CAG	CTG	GGG	CGC	1070
Asp	Gly	Ser	Gly	Pro	Tyr	Ser	Thr	Leu	Ser	Ser	Pro	Gln	Leu	Gly	Arg	
				80						85				90		
AGC	ACC	TAC	ATG	GAG	ACG	TAT	GTG	TAC	TTC	TAT	CGG	TCA	CAC	AAA	ACA	1118
Ser	Thr	Tyr	Met	Glu	Thr	Tyr	Val	Tyr	Phe	Tyr	Arg	Ser	His	Lys	Thr	
				95								105				
CAG	GTC	CTG	AGT	TCC	TAC	GTG	TAC	AAC	GAT	GAG	GAT	GAC	GTC	TTT	GCC	1166
Gln	Val	Leu	Ser	Ser	Tyr	Val	Tyr	Asn	Asp	Glu	Asp	Asp	Val	Phe	Ala	
		110					115				120					
CGG	GAG	CCA	TTT	GTG	GCC	CAG	TTC	TCT	TTG	CCC	AGC	AAT	GTC	CTT	CCC	1214
Arg	Glu	Pro	Phe	Val	Ala	Gln	Phe	Ser	Leu	Pro	Ser	Asn	Val	Leu	Pro	
		125				130				135					140	
AGC	CTG	GTG	TTG	GTC	CCG	CTG	CAC	ACC	ACT	CCT	AAG	GCC	GTA	GAG	AAG	1262
Ser	Leu	Val	Leu	Val	Pro	Leu	His	Thr	Thr	Pro	Lys	Ala	Val	Glu	Lys	
				145						150					155	

[illegible]

TGTAGTCTGT GTTGGTACAG GCTTCTGCAT GCCTGGTAAA GTCCAGCCAA GGCTGGTCAA	2350
GGCAACATCT CCACACAGAA AATCTGCACC AGTTATGTAA GCTAAAAAGC TGTGTGAACC	2410
CAGGTGTCCC GGAAAGGGGC TGCAGGACAC AGCAAAATGC CAGCAGCGTG CCGGACCCCT	2470
CCCTTCCATC CTCCTCTCCA AAGAACAGAG GTCAGGAAAA ACACTGGCTG GGACGCTAGA	2530
AGGGTCATGT GTTAACTATA ATCACATTTA TGGTTTGGAA CCATCACCCC AAGGTAAAAA	2590
AAAAAATAAA AGGTATGTTT GGCAAAATAA AATAAAGGTA ATTAAAAACC TAAAAAATAA	2650
AAAAAATAAA A	2661

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 Base pairs
 (B) TYPE: Nucleotide
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) TYPE OF MOLECULE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA-Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

CAGGGATCCG ATGACGATGA CAAAATGCAC TACCCAACTG CAC	43
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(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 Base pairs
 (B) TYPE: Nucleotide
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) TYPE OF MOLECULE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA-Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GGGGGATCCT CAGGCAGCAG GGCACAG	27
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